

SEQUENCE LISTING

<110> Lee, Se-Jin
McPherron, Alexandra C.

<120> GROWTH DIFFERENTIATION FACTOR RECEPTORS,
AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

<130> JHU1470-2

<150> 09/485,046
<151> 2000-01-31

<150> PCT/US98/15598
<151> 1998-07-28

<150> 60/054,461
<151> 1997-08-01

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<170> FastSEQ for Windows Version 4.0

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Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr					
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Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu					
65	70	75	80		
tta ccc aaa gct cct cca ctc cgg gaa ctg att gat cag tat gat gtc					346
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val					
85	90	95			

cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac	394
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
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gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt cta	442
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu	
115 120 125	
atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct	490
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Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
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Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
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Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
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Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys	
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tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca	1066
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
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<213> *Homo sapiens*

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Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
      35          40          45      .
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
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Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
      65          70          75          80
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
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Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
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Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu

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Arg Pro Val Glu Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu		160
165	170	175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu		
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Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val		
195	200	205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly		
210	215	220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr		
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Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys		240
245	250	255
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Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr		
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Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys		
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Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala		320
325	330	335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr		
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<222> (104) ... (1231)

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Met Met Gln Lys	
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ctg caa atg tat gtt tat att tac ctg ttc atg ctg att gct gct ggc	163		
Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile Ala Ala Gly			
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cca gtg gat cta aat gag ggc agt gag aga gaa aat gtg gaa aaa	211	
Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu Asn Val Glu Lys		
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gag ggg ctg tgt aat gca tgt gcg tgg aga caa aac acg agg tac tcc	259	
Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn Thr Arg Tyr Ser		
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gcg cct cca ctc cgg gaa ctg atc gat cag tac gac gtc cag agg gat	403
Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp	
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Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr	
105 110 115	
gaa aca atc att acc atg cct aca gag tct gac ttt cta atg caa gcg	499
Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala	
120 125 130	
gat ggc aag ccc aaa tgt tgc ttt ttt aaa ttt agc tct aaa ata cag	547
Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln	
135 140 145	
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Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg Pro Val	
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185 190 195	
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Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys Thr Val	
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Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr Phe Pro Gly	
230 235 240	
cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc aag gtg aca gac	883
Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys Val Thr Asp	
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aca ccc aag agg tcc cgg aga gac ttt ggg ctt gac tgc gat gag cac	931
Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His	
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<212> PRT
<213> *Mus musculus*

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 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125
 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160
 Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
 165 170 175
 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
 210 215 220
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
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96

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35	40	45	
aca agg tac tcc aga ata gaa gcc ata aaa att caa atc ctc agt aaa			192
Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys			
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ctc cgc ctg gaa aca gcg cct aac atc agc aaa gat gct ata aga caa			240
Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln			
65	70	75	80
ctt ctg ccc aga gcg cct cca ctc cgg gaa ctg atc gat cag tac gac			288
Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp			
85	90	95	
gtc cag agg gat gac agc agt gac ggc tct ttg gaa gat gac gat tat			336
Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr			
100	105	110	
cac gct acc acg gaa aca atc att acc atg cct acc gag tct gac ttt			384
His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe			
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cta atg caa gcg gat gga aag ccc aaa tgt tgc ttt ttt aaa ttt agc			432
Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser			
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Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val			
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Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270

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 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285

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 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300

tat aag gct aat tac tgc tct gga gag tgt gaa ttt gtg ttc tta caa
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320

aaa tat ccg cat act cat ctt gtg cac caa gca aac ccc aga ggc tcg
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335

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 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 340 345 350

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 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met
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<211> 376

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<213> Rattus norvegicus

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 35 40 45

Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60

Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80

Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95

Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr
 100 105 110

His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140

Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160

Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
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Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
 210 215 220
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
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<213> Gallus gallus

<220>

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 Ala Val Asp Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn
 20 25 30

gct gaa aaa gac gga ctg tgc aat gct tgt acg tgg aga cag aat aca 144
 Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45

aaa tcc tcc aga ata gaa gcc ata aaa att caa atc ctc agc aaa ctg 192
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 50 55 60

cgc ctg gaa caa gca cct aac att agc agg gac gtt att aag cag ctt 240
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 65 70 75 80

tta ccc aaa gct cct cca ctg cag gaa ctg att gat cag tat gat gtc 288
 Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95

cag agg gac gac agt agc gat ggc tct ttg gaa gac gat gac tat cat Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His 100 105 110	336
gcc aca acc gag acg att atc aca atg cct acg gag tct gat ttt ctt Ala Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu 115 120 125	384
gta caa atg gag gga aaa cca aaa tgt tgc ttc ttt aag ttt agc tct Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser 130 135 140	432
aaa ata caa tat aac aaa gta gta aag gca caa tta tgg ata tac ttg Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu 145 150 155 160	480
agg caa gtc caa aaa cct aca acg gtg ttt gtg cag atc ctg aga ctc Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu 165 170 175	528
att aag ccc atg aaa gac ggt aca aga tat act gga att cga tct ttg Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu 180 185 190	576
aaa ctt gac atg aac cca ggc act ggt atc tgg cag agt att gat gtg Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val 195 200 205	624
aag aca gtg ctg caa aat tgg ctc aaa cag cct gaa tcc aat tta ggc Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly 210 215 220	672
atc gaa ata aaa gct ttt gat gag act gga cga gat ctt gct gtc aca Ile Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr 225 230 235 240	720
ttc cca gga cca gga gaa gat gga ttg aac cca ttt tta gag gtc aga Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg 245 250 255	768
gtt aca gac aca ccg aaa cgg tcc cgc aga gat ttt ggc ctt gac tgt Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys 260 265 270	816
gat gag cac tca acg gaa tcc cga tgt tgt cgc tac ccg ctg aca gtg Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val 275 280 285	864
gat ttc gaa gct ttt gga tgg gac tgg att ata gca cct aaa aga tac Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr 290 295 300	912
aaa gcc aat tac tgc tcc gga gaa tgc gaa ttt gtg ttt cta cag aaa Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys 305 310 315 320	960
tac ccg cac act cac ctg gta cac caa gca aat ccc aga ggc tca gca Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala 325 330 335	1008

ggc cct tgc tgc aca ccc acc aag atg tcc cct ata aac atg ctg tat	1056		
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr			
340	345	350	
350			

ttc aat gga aaa gaa caa ata ata tat gga aag ata cca gcc atg gtt	1104		
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val			
355	360	365	
365			

gta gat cgt tgc ggg tgc tca tga	1128
Val Asp Arg Cys Gly Cys Ser	
370	375

<210> 8
 <211> 374
 <212> PRT
 <213> Gallus gallus

<400> 8	
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Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr Lys	
35 40 45	
Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg	
50 55 60	
Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu Leu	
65 70 75 80	
Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val Gln	
85 90 95	
Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala	
100 105 110	
Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Val	
115 120 125	
Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys	
130 135 140	
Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg	
145 150 155 160	
Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile	
165 170 175	
Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys	
180 185 190	
Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys	
195 200 205	
Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile	
210 215 220	
Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr Phe	
225 230 235 240	
Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg Val	
245 250 255	
Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp	
260 265 270	
Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp	
275 280 285	
Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys	
290 295 300	
Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr	
305 310 315 320	

Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly
 325 330 335
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val
 355 360 365
 Asp Arg Cys Gly Cys Ser
 370

<210> 9

<211> 1128

<212> DNA

<213> Baboon

<220>

<221> CDS

<222> (1)...(1125)

<400> 9

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 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
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gtt gct ggt cca gtg gat cta aat gag aac agt gag caa aaa gaa aat 96
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30

gtg gaa aaa gag ggg ctg tgt aat gca tgt act tgg aga caa aac act 144
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45

aaa tct tca aga ata gaa gcc att aaa ata caa atc ctc agt aaa ctt 192
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60

cgt ctg gaa aca gct cct aac atc agc aaa gat gct ata aga caa ctt 240
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80

tta ccc aaa gcg cct cca ctc cgg gaa ctg att gat cag tat gat gtc 288
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95

cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110

gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt tta 384
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125

atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct 432
 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140

aaa ata caa tac aat aaa gtg gta aag gcc caa cta tgg ata tat ttg 480
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160

aga ccc gtc gag act cct aca aca gtg ttt gtg caa atc ctg aga ctc 528

Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu			
165	170	175	
atc aaa cct atg aaa gac ggt aca agg tat act gga atc cga tct ctg		576	
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu			
180	185	190	
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg		624	
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val			
195	200	205	
aag aca gtg ttgcaa aat tgg ctc aaa caa cct gaa tcc aac tta ggc		672	
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly			
210	215	220	
att gaa ata aaa gct tta gat gag aat ggt cat gat ctt gct gta acc		720	
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr			
225	230	235	240
ttc cca gga cca gga gaa gat ggg ctg aat ccc ttt tta gag gtc aag		768	
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys			
245	250	255	
gta aca gac aca ccc aaa aga tcc aga agg gat ttt ggt ctt gac tgt		816	
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys			
260	265	270	
gat gag cac tca aca gaa tcg cga tgc tgt cgt tac cct cta act gtg		864	
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val			
275	280	285	
gat ttt gaa gct ctt gga tgg gat tgg att atc gct cct aaa aga tat		912	
Asp Phe Glu Ala Leu Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr			
290	295	300	
aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa		960	
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys			
305	310	315	320
tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca		1008	
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala			
325	330	335	
ggc cct tgc tgt act ccc aca aag atg tct cca att aat atg cta tat		1056	
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr			
340	345	350	
ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta		1104	
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val			
355	360	365	
gta gac cgc tgc ggg tgc tca tga		1128	
Val Asp Arg Cys Gly Cys Ser			
370	375		

<210> 10

<211> 375

<212> PRT

<213> Baboon

<400> 10
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 20 25 30
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Glu Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Leu Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 11

<211> 1128

<212> DNA

<213> Bovine

<220>

<221> CDS

<222> (1)...(1125)

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1 5 10 15		
gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat		96
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn		
20 25 30		
gtg gaa aaa gag ggg ctg tgt aat gca tgt ttg tgg agg gaa aac act		144
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr		
35 40 45		
aca tcg tca aga cta gaa gcc ata aaa atc caa atc ctc agt aaa ctt		192
Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu		
50 55 60		
cgc ctg gaa aca gct cct aac atc agc aaa gat gct atc aga caa ctt		240
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu		
65 70 75 80		
ttg ccc aag gct cct cca ctc ctg gaa ctg att gat cag ttc gat gtc		288
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val		
85 90 95		
cag aga gat gcc agc agt gac ggc tcc ttg gaa gac gat gac tac cac		336
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His		
100 105 110		
gcc agg acg gaa acg gtc att acc atg ccc acg gag tct gat ctt cta		384
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu		
115 120 125		
acg caa gtg gaa gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct		432
Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser		
130 135 140		
aag ata caa tac aat aaa cta gta aag gcc caa ctg tgg ata tat ctg		480
Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu		
145 150 155 160		
agg cct gtc aag act cct gcg aca gtg ttt gtg caa atc ctg aga ctc		528
Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu		
165 170 175		
atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg		576
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu		
180 185 190		
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg		624
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val		
195 200 205		
aag aca gtg ttg cag aac tgg ctc aaa caa cct gaa tcc aac tta ggc		672
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly		
210 215 220		
att gaa atc aaa gct tta gat gag aat ggc cat gat ctt gct gta acc		720
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr		
225 230 235 240		

ttc cca gaa cca gga gaa gat gga ctg act ccc ttt tta gaa gtc aag	768
Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys	
245 250 255	
gta aca gac aca cca aaa aga tct agg aga gat ttt ggg ctt gat tgt	816
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
260 265 270	
gat gaa cac tcc aca gaa tct cga tgc tgt cgt tac cct cta act gtg	864
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
275 280 285	
gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat	912
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	
290 295 300	
aag gcc aat tac tgc tct gga gaa tgt gaa ttt gta ttt ttg caa aag	960
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys	
305 310 315 320	
stat cct cat acc cat ctt gtg cac caa gca aac ccc aga ggt tca gcc	1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
325 330 335	
ggc ccc tgc tgt act cct aca aag atg tct cca att aat atg cta tat	1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr	
340 345 350	
ttt aat ggc gaa gga caa ata ata tac ggg aag att cca gcc atg gta	1104
Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val	
355 360 365	
gta gat cgc tgt ggg tgt tca tga	1128
Val Asp Arg Cys Gly Cys Ser	
370 375	
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20 25 30	
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr	
35 40 45	
Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu	
65 70 75 80	
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val	
85 90 95	
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
100 105 110	
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu	
115 120 125	

Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 13

<211> 1128

<212> DNA

<213> Porcine

<220>

<221> CDS

<222> (1) ... (1125)

<400> 13

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gtt gct ggt ccc gtg gat ctg aat gag aac agc gag caa aag gaa aat 96
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30

gtg gaa aaa gag ggg ctg tgt aat gca tgt atg tgg aga caa aac act 144
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr
 35 40 45

aaa tct tca aga cta gaa gcc ata aaa att caa atc ctc agt aaa ctt 192
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60

cgc ctg gaa aca gct cct aac att agc aaa gat gct ata aga caa ctt 240

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80

ttg ccc aaa gct cct cca ctc cg^g gaa ctg att gat cag tac gat gtc 288
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95

cag aga gat gac agc agt gat ggc tcc ttg gaa gat gat gat tat cac 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110

gct acg acg gaa acg atc att acc atg cct aca gag tct gat ctt cta 384
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125

atg caa gtg gaa gga aaa ccc aaa tgc tgc ttc ttt aaa ttt agc tct 432
 Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140

aaa ata caa tac aat aaa gta gta aag gcc caa ctg tgg ata tat ctg 480
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160

aga ccc gtc aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc 528
 Arg Pro Val Lys Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175

atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg 576
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190

aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg 624
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205

aag aca gtg ttg caa aat tgg ctc aaa caa cct gaa tcc aac tta ggc 672
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220

att gaa atc aaa gct tta gat gag aat ggt cat gat ctt gct gta acc 720
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240

ttc cca gga cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc aag 768
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255

gta aca gac aca cca aaa aga tcc agg aga gat ttt gga ctc gac tgt 816
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

gat gag cac tca aca gaa tct cga tgc tgt cgt tac cct cta act gtg 864
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285

gat ttt gaa gct ttt gga tgg gac tgg att att gca ccc aaa aga tat 912
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300

aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa 960

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys				
305	310	315	320	
tac cct cac act cat ctt gtg cac caa gca aac ccc aga ggt tca gca				1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala				
325	330	335		
ggc ccc tgc tgt act ccc aca aag atg tct cca atc aat atg cta tat				1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr				
340	345	350		
ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta				1104
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val				
355	360	365		
gta gat cgc tgt ggg tgc tca tga				1128
Val Asp Arg Cys Gly Cys Ser				
370	375			

<210> 14

<211> 375

<212> PRT

<213> Porcine

<400> 14

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20	25	30		
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr				
35	40	45		
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu				
50	55	60		
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu				
65	70	75	80	
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val				
85	90	95		
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His				
100	105	110		
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu				
115	120	125		
Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser				
130	135	140		
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu				
145	150	155	160	
Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu				
165	170	175		
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu				
180	185	190		
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val				
195	200	205		
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly				
210	215	220		
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr				
225	230	235	240	
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys				
245	250	255		
Val Thr Asp Thr Pro Lys Arg Ser Arg Asp Phe Gly Leu Asp Cys				
260	265	270		

Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 15
 <211> 1128
 <212> DNA
 <213> Ovine

<220>

<221> CDS
 <222> (1) ... (1125)

<400> 15

atg caa aaa ctg caa atc ttt gtt tat att tac cta ttt atg ctg ctt 48
 Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
 1 5 10 15

gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat 96
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30

gtg gaa aaa aag ggg ctg tgt aat gca tgc ttg tgg aga caa aac aat 144
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
 35 40 45

aaa tcc tca aga cta gaa gcc ata aaa atc caa atc ctc agt aag ctt 192
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60

cgc ctg gaa aca gct cct aac atc agc aaa gat gct ata aga caa ctt 240
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80

ttg ccc aag gct cct cca ctc cgg gaa ctg att gat cag tac gat gtc 288
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95

cag aga gat gac agc gac gac ggc tcc ttg gaa gac gat gac tac cac 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110

gtt acg acg gaa acg gtc att acc atg ccc acg gag tct gat ctt cta 384
 Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125

gca gaa gtg caa gaa aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct 432
 Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140

aag ata caa cac aat aaa gta gta aag gcc caa ctg tgg ata tat ctg Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu 145 150 155 160	480
aga cct gtc aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc Arg Pro Val Lys Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu 165 170 175	528
atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu 180 185 190	576
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val 195 200 205	624
aag aca gtg ttg caa aac tgg ctc aaa caa cct gaa tcc aac tta ggc Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly 210 215 220	672
att gaa atc aaa gct tta gat gag aat ggt cat gat ctt gct gta acc Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr 225 230 235 240	720
ttc cca gaa cca gga gaa gga ctg aat cct ttt tta gaa gtc aag Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys 245 250 255	768
gta aca gac aca cca aaa aga tct agg aga gat ttt ggg ctt gat tgt Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys 260 265 270	816
gat gag cac tcc aca gaa tct cga tgc tgt cgt tac cct cta act gtg Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val 275 280 285	864
gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr 290 295 300	912
aag gcc aat tac tgc tct gga gaa tgt gaa ttt tta ttt ttg caa aag Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys 305 310 315 320	960
tat cct cat acc cat ctt gtg cac caa gca aac ccc aaa ggt tca gcc Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala 325 330 335	1008
ggc cct tgc tgt act cct aca aag atg tct cca att aat atg cta tat Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr 340 345 350	1056
ttt aat ggc aaa gaa caa ata ata tat ggg aag att cca ggc atg gta Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val 355 360 365	1104
gta gat cgc tgt ggg tgc tca tga Val Asp Arg Cys Gly Cys Ser 370 375	1128

<210> 16
 <211> 375
 <212> PRT
 <213> Ovine

<400> 16
 Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
 1 5 10 15
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
 35 40 45
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125
 Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 17
 <211> 1128
 <212> DNA

<213> Meleagris gallopavo

<220>

<221> CDS

<222> (1)...(1125)

<400> 17

atg caa aag cta gca gtc tat gtt tat att tac ctg ttc atg cag att	48
Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile	
1 5 10 15	

tta gtt cat ccg gtg gct ctt gat ggc agt agt cag ccc aca gag aac	96
Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn	
20 25 30	

gct gaa aaa gac gga ctg tgc aat gct tgc acg tgg aga cag aat act	144
Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr	
35 40 45	

aaa tcc tcc aga ata gaa gcc ata aaa att caa atc ctc agc aaa ctg	192
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	

ccg ctg gaa caa gca cct aac att agc agg gac gtt att aaa caa ctt	240
Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu	
65 70 75 80	

tta ccc aaa gct cct ccg ctg cag gaa ctg att gat cag tat gac gtc	288
Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val	
85 90 95	

cag aga gac gac agt agc gat ggc tct ttg gaa gac gat gac tat cat	336
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
100 105 110	

gcc aca acc gaa acg att atc aca atg cct acg gag tct gat ttt ctt	384
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu	
115 120 125	

gta caa atg gag gga aaa cca aaa tgt tgc ttc ttt aag ttt agc tct	432
Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	
130 135 140	

aaa ata caa tat aac aaa gta gta aag gca caa tta tgg ata tac ttg	480
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu	
145 150 155 160	

agg caa gtc caa aaa cct aca acg gtg ttt gtg cag atc ctg aga ctc	528
Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu	
165 170 175	

att aaa ccc atg aaa gac ggt aca aga tat act gga att cga tct ttg	576
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
180 185 190	

aaa ctt gac atg aac cca ggc act ggt atc tgg cag agt att gat gtg	624
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
195 200 205	

aag aca gtg ttg caa aat tgg ctc aaa cag cct gaa tcc aat tta ggc	672
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25

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220

atc gaa ata aaa gct ttt gat gag aat gga cga gat ctt gct gta aca 720
 Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr
 225 230 235 240

ttc cca gga cca ggt gaa gat gga ctg aac cca ttt tta gag gtc aga 768
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
 245 250 255

gtt aca gac aca cca aaa cg^g tcc cg^c aga gat ttt gg^c ctt gac tg^c 816
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

gac gag cac tca acg gaa tct cga tgt tgt cgc tac ccg ctg aca gtg 864
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285

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gat ttt gaa gct ttt gga tgg gac tgg att ata gca cct aaa aga tac 912
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
         290          295          300

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aaa gcc aat tac tgc tct gga gaa tgt gaa ttc gta ttt cta cag aaa      960
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
305          310          315          320

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tac ccg cac act cac ctg gta cac caa gca aat cca aga ggc tca gca      1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
325          330          335

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ggc cct tgc tgc aca ccc acc aag atg tcc cct ata aac atg ctg tat      1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
          340          345          350
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ttc aat gga aaa gaa caa ata ata tat gga aag ata cca gcc atg gtt      1104
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
...          355          360          365

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gta gat cgt tgc ggg tgc tca tga 1128
Val Asp Arg Cys Gly Cys Ser
370 375

<210> 18
<211> 375
<212> PRT
<213> Meleagris gallopavo

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<400> 18
Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile
      5          10          15
Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn
      20          25          30
Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
      35          40          45
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
      50          55          60
Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu
65          70          75          80

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Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 19
 <211> 1125
 <212> DNA
 <213> Danio rerio

<220>
 <221> CDS
 <222> (1)...(1122)

<400> 19
 atg cat ttt aca cag gtt tta att tct cta agt gta tta att gca tgt
 Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys
 1 5 10 15 48
 ggt cca gtg ggt tat gga gat ata acg gcg cac cag cag cct tcc aca
 Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr
 20 25 30 96
 gcc acg gag gaa agc gag ctg tgt tcc aca tgt gag ttc aga caa cac
 Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His
 35 40 45 144

agc aag ctg atg aga ctg cat gcc atc aag tcc caa att ctt agc aaa Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys 50 55 60	192
ctc cga ctc aag cag gct cca aac atc agc cgg gac gtc gtc aag cag Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln 65 70 75 80	240
ctg tta ccc aaa gca ccg cct ttg caa caa ctt ctg gat cag tac gat Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp 85 90 95	288
gtt tta gga gat gac agt aag gat gga gct gtc gaa gag gac gat gaa Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu 100 105 110	336
cat gcc acc aca gag acc atc atg acc atg gcc aca gaa cct gac ccc His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro 115 120 125	384
att gtt caa gta gat cgg aaa ccg aag tgt tgc ttt ttc tcc ttc agt Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser 130 135 140	432
ccg aag atc caa gcg aac ccg atc gta aga gcg cag ctc tgg gtt cat Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His 145 150 155 160	480
ctg aga ccg gcg gag gag gcg acc acc gtc ttc tta cag ata tct cgg Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg 165 170 175	528
ctg atg ccc gtt aag gac gga gga aga cac cga ata cga tcc ctg aaa Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys 180 185 190	576
atc gac gtg aac gca gga gtc acg tct tgg cag agt ata gac gta aag Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys 195 200 205	624
cag gtg ctc acg gtg tgg tta aaa caa ccg gag acc aac cga ggc atc Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile 210 215 220	672
gag att aac gca tat gac gcg aag gga aac gac ttg gcc gtc act tca Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser 225 230 235 240	720
acc gag act ggg gag gat gga ctg ctc ccc ttt atg gag gtg aaa ata Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile 245 250 255	768
tca gag ggc cca aaa cga atc cgg agg gac tcc gga ctg gac tgc gat Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp 260 265 270	816
gag aat tcc tca gag tct cgc tgc tgc agg tac cct ctc act gtg gac Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp 275 280 285	864

ttc gag gac ttt ggc tgg gac tgg att att gct cca aaa cgc tat aag Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys 290 295 300	912
gcg aat tac tgt tca gga gaa tgc gac tac atg tac ctg cag aag tat Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr 305 310 315 320	960
ccc cac acc cat ctg gtg aac aag gcc agt ccg aga gga acg gct ggg Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly 325 330 335	1008
ccc tgc tgc act ccc acc aag atg tct ccc atc aac atg ctt tac ttt Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe 340 345 350	1056
aac ggc aaa gag cag atc atc tac ggc aag atc cct tcg atg gta gta Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val 355 360 365	1104
gac cgc tgt ggc tgc tca tga Asp Arg Cys Gly Cys Ser 370	1125

<210> 20
 <211> 374
 <212> PRT
 <213> Danio rerio

Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys 1 5 10 15
Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr 20 25 30
Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His 35 40 45
Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys 50 55 60
Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln 65 70 75 80
Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp 85 90 95
Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu 100 105 110
His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro 115 120 125
Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser 130 135 140
Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His 145 150 155 160
Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg 165 170 175
Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys 180 185 190
Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys 195 200 205
Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile 210 215 220

Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser
 225 230 235 240
 Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile
 245 250 255
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp
 260 265 270
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp
 275 280 285
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys
 290 295 300
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr
 305 310 315 320
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly
 325 330 335
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val
 355 360 365
 Asp Arg Cys Gly Cys Ser
 370

<210> 21

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> proteolytic cleavage site

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Any Amino Acid

<400> 21

Arg Xaa Xaa Arg

1

<210> 22

<211> 4

<212> PRT

<213> Eukaryotes

<220>

<221> SITE

<222> (0)...(0)

<223> proteolytic processing site

<400> 22

Arg Ser Arg Arg

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<210> 23

<211> 4

<212> PRT

<213> Eukaryotes

<220>

<221> SITE

<222> (0)...(0)

<223> proteolytic processing site

<400> 23
 Arg Ile Arg Arg
 1

 <210> 24
 <211> 1393
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (54) ... (1274)
 <223> GDF-11

 <400> 24
 ccgcgggact cccggcgtccc cgcgcgcgcag tcctccctcc cctccctcc agc atg 56
Met
1

 gtg ctc gcg gcc ccg ctg ctg ggc ttc ctg ctc ctc gcc ctg gag 104
 Val Leu Ala Ala Pro Leu Leu Leu Gly Phe Leu Leu Leu Ala Leu Glu
5 10 15

 ctg cgg ccc cgg ggg gag gcg gcc gag ggc ccc gcg gcg gcg gcg 152
 Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala Ala
20 25 30

 gcg gcg gcg gcg gca gcg gcg ggg gtc ggg ggg gag cgc tcc agc 200
 Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser Ser
35 40 45

 cgg cca gcc ccg tcc gtg gcg ccc gag ccg gac ggc tgc ccc gtg tgc 248
 Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val Cys
50 55 60 65

 gtt tgg cgg cag cac agc cgc gag ctg cgc cta gag agc atc aag tcg 296
 Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys Ser
70 75 80

 cag atc ttg agc aaa ctg cgg ctc aag gag gcg ccc aac atc agc cgc 344
 Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser Arg
85 90 95

 gag gtg gtg aag cag ctg ctg ccc aag gcg ccc ccc ctg cag cag atc 392
 Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Ile
100 105 110

 ctg gac cta cac gac ttc cag ggc gac gcg ctg cag ccc gag gac ttc 440
 Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp Phe
115 120 125

 ctg gag gag gac gag tac cac gcc acc acc gag acc gtc att agc atg 488
 Leu Glu Glu Asp Glu Tyr His Ala Thr Thr Glu Thr Val Ile Ser Met
130 135 140 145

 gcc cag gag acg gac cca gca gta cag aca gat ggc agc cct ctc tgc 536
 Ala Gln Glu Thr Asp Pro Ala Val Gln Thr Asp Gly Ser Pro Leu Cys
150 155 160

tgc cat ttt cac ttc agc ccc aag gtg atg ttc aca aag gta ctg aag	584
Cys His Phe His Phe Ser Pro Lys Val Met Phe Thr Lys Val Leu Lys	
165 170 175	
gcc cag ctg tgg gtg tac cta cgg cct gta ccc cgc cca gcc aca gtc	632
Ala Gln Leu Trp Val Tyr Leu Arg Pro Val Pro Arg Pro Ala Thr Val	
180 185 190	
tac ctg cag atc ttg cga cta aaa ccc cta act ggg gaa ggg acc gca	680
Tyr Leu Gln Ile Leu Arg Leu Lys Pro Leu Thr Gly Glu Gly Thr Ala	
195 200 205	
ggg gga ggg ggc gga ggc cgg cgt cac atc cgt atc cgc tca ctg aag	728
Gly Gly Gly Gly Gly Arg Arg His Ile Arg Ile Arg Ser Leu Lys	
210 215 220 225	
att gag ctg cac tca cgc tca ggc cat tgg cag agc atc gac ttc aag	776
Ile Glu Leu His Ser Arg Ser Gly His Trp Gln Ser Ile Asp Phe Lys	
230 235 240	
caa gtg cta cac agc tgg ttc cgc cag cca cag agc aac tgg ggc atc	824
Gln Val Leu His Ser Trp Phe Arg Gln Pro Gln Ser Asn Trp Gly Ile	
245 250 255	
gag atc aac gcc ttt gat ccc agt ggc aca gac ctg gct gtc acc tcc	872
Glu Ile Asn Ala Phe Asp Pro Ser Gly Thr Asp Leu Ala Val Thr Ser	
260 265 270	
ctg ggg cgc gga gcc gag ggg ctg cat cca ttc atg gag ctt cga gtc	920
Leu Gly Pro Gly Ala Glu Gly Leu His Pro Phe Met Glu Leu Arg Val	
275 280 285	
cta gag aac aca aaa cgt tcc cgg cgg aac ctg ggt ctg gac tgc gac	968
Leu Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys Asp	
290 295 300 305	
gag cac tca agc gag tcc cgc tgc cga tat ccc ctc aca gtg gac	1016
Glu His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp	
310 315 320	
ttt gag gct ttc ggc tgg gac tgg atc atc gca cct aag cgc tac aag	1064
Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys	
325 330 335	
gcc aac tac tgc tcc ggc cag tgc gag tac atg ttc atg caa aaa tat	1112
Ala Asn Tyr Cys Ser Gly Gln Cys Glu Tyr Met Phe Met Gln Lys Tyr	
340 345 350	
ccg cat acc cat ttg gtg cag cag gcc aat cca aga ggc tct gct ggg	1160
Pro His Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala Gly	
355 360 365	
ccc tgt tgt acc ccc acc aag atg tcc cca atc aac atg ctc tac ttc	1208
Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe	
370 375 380 385	
aat gac aag cag cag att atc tac ggc aag atc cct ggc atg gtg gtg	1256
Asn Asp Lys Gln Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val Val	
390 395 400	

gat cgc tgt ggc tgc tct taagtgggtc actacaagct gctggagcaa 1304
 Asp Arg Cys Gly Cys Ser
 405

agacttggtg ggtggtaac ttaaccttt cacagaggat aaaaaatgct tgtgagtag 1364
 acagaaggga ataaacaggc ttaaagggt 1393

<210> 25
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Val Leu Ala Ala Pro Leu Leu Leu Gly Phe Leu Leu Ala Leu
 1 5 10 15
 Glu Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala
 20 25 30
 Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser
 35 40 45
 Ser Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val
 50 55 60
 Cys Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys
 65 70 75 80
 Ser Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser
 85 90 95
 Arg Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln
 100 105 110
 Ile Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp
 115 120 125
 Phe Leu Glu Glu Asp Glu Tyr His Ala Thr Thr Glu Thr Val Ile Ser
 130 135 140
 Met Ala Gln Glu Thr Asp Pro Ala Val Gln Thr Asp Gly Ser Pro Leu
 145 150 155 160
 Cys Cys His Phe His Phe Ser Pro Lys Val Met Phe Thr Lys Val Leu
 165 170 175
 Lys Ala Gln Leu Trp Val Tyr Leu Arg Pro Val Pro Arg Pro Ala Thr
 180 185 190
 Val Tyr Leu Gln Ile Leu Arg Leu Lys Pro Leu Thr Gly Glu Gly Thr
 195 200 205
 Ala Gly Gly Gly Gly Arg Arg His Ile Arg Ile Arg Ser Leu
 210 215 220
 Lys Ile Glu Leu His Ser Arg Ser Gly His Trp Gln Ser Ile Asp Phe
 225 230 235 240
 Lys Gln Val Leu His Ser Trp Phe Arg Gln Pro Gln Ser Asn Trp Gly
 245 250 255
 Ile Glu Ile Asn Ala Phe Asp Pro Ser Gly Thr Asp Leu Ala Val Thr
 260 265 270
 Ser Leu Gly Pro Gly Ala Glu Gly Leu His Pro Phe Met Glu Leu Arg
 275 280 285
 Val Leu Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys
 290 295 300
 Asp Glu His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 305 310 315 320
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 325 330 335
 Lys Ala Asn Tyr Cys Ser Gly Gln Cys Glu Tyr Met Phe Met Gln Lys
 340 345 350
 Tyr Pro His Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala
 355 360 365
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr

370	375	380
Phe Asn Asp Lys Gln Gln	Ile Ile Tyr Gly Lys	Ile Pro Gly Met Val
385	390	395
Val Asp Arg Cys Gly Cys Ser		
	405	

<210> 26
<211> 476
<212> DNA
<213> Salmon-1

<220>
<221> CDS
<222> (3) . . . (473)

<400> 26
gg cag ccg gag acg aat tgg ggg atc gag att aat gag ttc gac tcg 47
Gln Pro Glu Thr Asn Trp Gly Ile Glu Ile Asn Ala Phe Asp Ser
1 5 10 15

aag gga aat gat ctg gcc gtt acc tca gca gaa gcg gga gaa gga ctg 95
 Lys Gly Asn Asp Leu Ala Val Thr Ser Ala Glu Ala Gly Glu Gly Leu
 20 25 30

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caa ccc ttc atg gag gtg acg att tca gag ggc ccg aag cgc tcc agg 143
Gln Pro Phe Met Glu Val Thr Ile Ser Glu Gly Pro Lys Arg Ser Arg
          35           40           45

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aga gac tcg ggc ctg gac tgt gac gag aac tcc ccc gag tcc cgc tgt 191
Arg Asp Ser Gly Leu Asp Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys
      50           55           60

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tgc cgc tac ccc ctc acg gta gac ttt gaa gac ttt ggc tgg gac tgg 239
 Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Asp Phe Gly Trp Asp Trp
 65 70 75

att att gcc ccc aag cgc tac aag gcc aac tac tgc tct ggt gag tgt
 Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys
 80 85 90 95 287

gag tac atg cac ctg cag aag tac ccc cac acc cac ctg gtg aac aag 335
 Glu Tyr Met His Leu Gln Lys Tyr Pro His Thr His Leu Val Asn Lys
 100 105 110

gct aac cct cgc ggc acc gca ggg ccc tgc tgc acc ccc acc aag atg 383
 Ala Asn Pro Arg Gly Thr Ala Gly Pro Cys Cys Thr Pro Thr Lys Met
 115 120 125

tcc ccc atc aac atg ctc tac ttc aac cgc aaa gag cag atc atc tac	431
Ser Pro Ile Asn Met Leu Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr	
130 135 140	

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ggc aag atc ccc tcc atg gtg gtg gac cgt tgc gga tgc tcg 473
Gly Lys Ile Pro Ser Met Val Val Asp Arg Cys Gly Cys Ser
    145           150           155

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tga 476

<212> PRT
<213> Salmon-1

<400> 27

Gln	Pro	Glu	Thr	Asn	Trp	Gly	Ile	Glu	Ile	Asn	Ala	Phe	Asp	Ser	Lys
1					5				10					15	
Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser	Ala	Glu	Ala	Gly	Glu	Gly	Leu	Gln
					20				25					30	
Pro	Phe	Met	Glu	Val	Thr	Ile	Ser	Glu	Gly	Pro	Lys	Arg	Ser	Arg	Arg
					35			40			45				
Asp	Ser	Gly	Leu	Asp	Cys	Asp	Glu	Asn	Ser	Pro	Glu	Ser	Arg	Cys	Cys
					50			55			60				
Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile
65					70				75					80	
Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu
					85				90					95	
Tyr	Met	His	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala
					100			105					110		
Asn	Pro	Arg	Gly	Thr	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
					115			120			125				
Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Arg	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
					130			135			140				
Lys	Ile	Pro	Ser	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser			
145					150				155						

<210> 28

<211> 412

<212> DNA

<213> Salmon-2

<220>

<221> CDS

<222> (2) . . . (409)

<400> 28

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Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val
1 5 10 15

aag att tcg gag ggc ccg aag cgc tcc agg aga gat tcg ggc ctg gac 97
 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp
 20 25 30

tgt gat gag aac tcc ccc gag tcc cgc tgc tgc cgg tac ccc ctc acg
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 35 40 45 145

gtg gac ttt gaa gac ttt ggc tgg gac tgg att att gcc ccc aag cgc 193
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 50 55 60

tac aag gcc aac tac tgc tct ggt gag tgc gag tac atg cac ctg cag 241
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln
 65 70 75 80

aag tac ccc cac acc cac ctg gtg aac aag gct aac cct cgc ggc acc 289
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr
 85 90 95

ggg ggg ccc tgc tgc acc ccc acc aag atg tcc ccc atc aac atg ctc 337

Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 100 105 110

tac ttc aac cgc aaa gag cag atc atc tac ggc aag atc ccc tcc atg 385
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met
 115 120 125

gtg gtg gac cgc tgc ggc tgc tcg tga 412
 Val Val Asp Arg Cys Gly Cys Ser
 130 135

<210> 29
 <211> 136
 <212> PRT
 <213> Salmon-2

<400> 29
 Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val
 1 5 10 15
 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp
 20 25 30
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 35 40 45
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 50 55 60
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln
 65 70 75 80
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr
 85 90 95
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 100 105 110
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met
 115 120 125
 Val Val Asp Arg Cys Gly Cys Ser
 130 135